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DEC 8 2000

NOV 27 2000

Sequence Listing

<110> ASHKENAZI, AVI J
BOTSTEIN, DAVID
DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val
1 5 10 15

Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
20 25 30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
35 40 45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
50 55 60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
65 70 75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
80 85 90

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	
				95					100					105	
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	
				110					115					120	
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	
				125					130					135	
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	
				140					145					150	
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	
				155					160					165	
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	
				170					175					180	
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	
				185					190					195	
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	
				200					205					210	
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	
				215					220					225	
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	
				230					235					240	
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	
				245					250					255	
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	
				260					265					270	
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	
				275					280					285	
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	
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<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggt caggcacagc 50
agggtcctgt gtccgcgctg agccgcgctc tccttctctc agcaaggacc 100
atgagggcgc tggaggggccc aggctgtcgc ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgctgc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
cggcttcttc gcgcacgctg gtttctgctt ggagcaagca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc cccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggttcccc 700
ctcagcacca ggggtaccag agctgaggag tgtgagcgtg ccgtcatoga 750
ctttgtggct ttccaggaca tctccatcaa gaggtgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850
gcggccttgc agctgaagct gcgtcggcgg ctacaggagc tcctgggggc 900
gcaggacggg gcgctgctgg tgccgctgct gcaggcgtg cgcgtggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttctct cctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac ccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

<400> 3
gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50
cagttctgga antaactgga gcncctgccg tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150
gccgctgccg caccggcttc ttccgcacg ctggttttctg cttggagcac 200
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 250
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300
tccagctcag agcagtgccg gccccaccgc aactgcacgg ccctgggcct 350
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
gcactggctt cccctcagc accagggtag caggagctga ggagtgtgag 450
cgtgcgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag cccacgacg tgtggcccg gtccaccgcn actacacg 50

cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gcnctgcag caccggnctt ttcgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncgcggca cccacagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgtgcc gcaccggctt cttcgcgcac gctgggttct gcttgagca 150

cgcacgtgt ccacctggtg ccggcgtgat tncgccgggc accccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 142

<223> unknown base

<400> 7

gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgct 50

ggtcccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100

cttcctctct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150

gccccccagg cacctttctca gccagcagct ccagctcaga gcagtgccag 200

ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250

ttcttcccat gacacctgt gcaccag 277

<210> 8

<211> 199

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 8

gcatcgtgtc cacctgggtg cggcgtgatt gccccgggca cccccagcca 50

gaacacgcag gcctagccgt gccccccagg cacctttctca gccagcagct 100

ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150

gccctcaatg tgccaggctc ttcttcccat gacacctgt gcaccagct 199

<210> 9

<211> 226

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 4, 9, 12, 165

<223> unknown base

<400> 9

agcngtgcnc encaggcacc ttctcagcca gcagttccag ctgagagcag 50

tgccagcccc accgcaactg cacggccctg ggcttgcccc tcaatgtgcc 100
aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
tttgtggctt tccaggacat ctccat 226

<210> 10
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 1-283
<223> Unknown organism

<220>
<221> unsure
<222> 27, 64, 140
<223> unknown base

<400> 10
cttgtccacc tgggtgccggc gtgattnccc gggcaccccc agccagaaca 50
cgcagtgcc a gcentcccc caggcacctt ctcagccagc agtccagct 100
cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150
atgtgccagg ctcttctctcc catgacaccc tgtgcaccag ctgcactggc 200
ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250
catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
<211> 21
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 11
cacgctgggt tctgcttgga g 21

<210> 12
<211> 22
<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

cttcttcgcg cacgctg 17

<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu
1 5 10 15
Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
20 25 30
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
35 40 45
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
50 55 60
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
65 70 75
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
80 85 90
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
95 100 105
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
110 115 120
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
125 130 135
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
140 145 150
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
155 160 165
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
170 175 180
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
185 190 195
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
200 205 210

Pro Gly Ala Val	His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln	215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val Asn Cys Val Ile Met Thr	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu	425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro	440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys Pro Ser	455	460	

<210> 18
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 1 5 10 15
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 20 25 30
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 35 40 45
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 50 55 60
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 65 70 75
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 80 85 90
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 95 100 105
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 110 115 120
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 125 130 135
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 140 145 150
 Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 155 160 165
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 170 175 180
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
 185 190 195
 Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
 200 205 210
 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
 215 220 225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
275 280 285

Gly His Ala Asn Leu Thr Phe Glu
290